

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/574,297
Source: IFWP
Date Processed by STIC: 4/17/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/17/2006

PATENT APPLICATION: US/10/574,297

TIME: 12:22:57

Input Set : N:\DA\PTO.DA.txt

Output Set: N:\CRF4\04172006\J574297.raw

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4 <110> APPLICANT: CASTADO, Cindy
5      DENOEL, Philippe
6      GODFROID, Fabrice
7      POOLMAN, Jan
9 <120> TITLE OF INVENTION: PERTUSSIS ANTIGENS AND USE THEREOF IN
10     VACCINATION
12 <130> FILE REFERENCE: VB60452
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/574,297
15 <141> CURRENT FILING DATE: 2006-03-31
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/011082
18 <151> PRIOR FILING DATE: 2004-10-01
20 <150> PRIOR APPLICATION NUMBER: GB 0323113.1
21 <151> PRIOR FILING DATE: 2003-10-02
23 <150> PRIOR APPLICATION NUMBER: GB 0323112.3
24 <151> PRIOR FILING DATE: 2003-10-02
26 <160> NUMBER OF SEQ ID NOS: 110
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2214
32 <212> TYPE: DNA
33 <213> ORGANISM: Bordetella Pertussis
35 <400> SEQUENCE: 1
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37 ggccctggcca tggcgagac gccacccag atccacgac cgctcgaggt gcagcagatg 120
38 gcgacggtgc aggtgctggg caccggccgaa gaggaaatca aggagtcgct gggcgctctcg 180
39 gtcacacccg ccgaggagat cggccgcgc cggccacca atgacctgct cgacctgac 240
40 cgccgcgaac ccggcgtaa cctgaccggc aacagcgcca gcggcgcgcg gggcaacagc 300
41 cgccaggctc acatccgcgg catgggccc gagaacaccc tcacacctgat cgacggcaag 360
42 cccgtcacct cgcgcaatgc ggtgcgtat ggctggaac gcgaccggga cacgcgcggg 420
43 gacaccaact ggggtcccgc cgaggaaatc gagcgcatcg aagtgatccg cggcccggcc 480
44 gccgcccgtc acggttccgg ggccatgggc ggcgtggta acatcatcac caagcgcccc 540
45 gccgatcgcg ccaccggctc catcacctac tacacgaacc agccggaaga cagccgcgag 600
46 ggcaaacacca accgcgtcaa tgcgcgcac agcgcgccga tcagcgacac gctgagcatg 660
47 cggtgttacg gcaactacaa caagaccaat ccggatgccc gcgacatcaa cgccggccac 720
48 gcgaacacca gcgacaacgg caaccctcgc accgccggac gcgagggcgt catcaaccag 780
49 gacctgagcg cgctgttctc gtggaaaagg gacagccaca acaccgtgga cctggacatg 840
50 ggcttcagcc ggcagggcaa cctgttcgcc ggcgacacca tgaacaacgc caacagcgac 900
51 ttctcggaca gcctgtacgg caaggaaacc aatgcgatgt accgcgagaa ctatgcgctg 960
52 acgcaccgcg gcgtctacga ctggggcacc tcgcgcgcca gcgtcggcta tgactacacg 1020
53 cgcaacgcgc gccagcgca aggcctggcc ggcggcccc agggcgcgcc caccgcgggc 1080
54 ggctacgcga ccgcgcgct gaagaactgg ccgcccgcgg ccgaggccag cgtgccgttc 1140
55 catctcggtt tcgagcaggt cgccacgggt ggcgtggaat ggctgcgcga atcgctggaa 1200
56 gaccccgccg gcacgcgcca gacctatacc ggcggcgcca tcggcgccac ggccccggcc 1260

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57 gaccgcgacc cgaaatcgcg ccagaccagc tatgcgctgt tcgccgagga caacatcgag 1320
58 atcgacgagc gcaccatgct cagccccggc gtgcgcctgg accacaacag cgaattcggc 1380
59 agcaactgga gtcccagcct gaacgcctcg tacgcgcgtca ccgacgcgct caagctcaag 1440
60 ggtggcatcg cgcgcgccta caaggcgccc aacctctacc aatccaaccc caactacctg 1500
61 ctgtacagcc gcggcaatgg ctgcctggcc tcgcagacca acaccaacgg ctgctatctg 1560
62 gtcggcaacg aggacctctc gccggaaacc agcgtcaaca aggaaatcgg cttcgagtac 1620
63 gacccgggca cgtggcgcac cagcatggcc tatttccgca acgactaccg caacaagatc 1680
64 gtcgccggca ccgacgtcca gtaccgcctg gccaatggcg cccgggtgct gcaatggacc 1740
65 aacagcggca aggcctgggt cgaagggtcg gaaggcaacc tggtcattcc gctggccagc 1800
66 aatctcgact ggaacaccaa cttcacctac atgatccagt ccaaggaaaa ggctaccggc 1860
67 gaacccttga gcgtgattcc cgaatacacc atcaacagca cgctggactg gttctacacg 1920
68 ccgcagctgt cgttccaggc caatctcacc tattacggca agcaggaagg cccgtccacc 1980
69 aatgtacgca ccggcgctga actgaacggc gacggccgcc agaccatcag tccgtatgcc 2040
70 ctggcggggc tgagcatggg ctacgaagtc aaccggaacc tgaagttccg cgtcggcgctg 2100
71 agcaacctgt tcgacaagca gctgtaccgc gaaggcaatg ccagcagcgc gggcgcgggc 2160
72 acctacaacg aaccggggcg cgcctattac gccacggcga cggtgtcggt ctga 2214

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74 <210> SEQ ID NO: 2

75 <211> LENGTH: 737

76 <212> TYPE: PRT

77 <213> ORGANISM: Bordetella Pertussis

79 <400> SEQUENCE: 2

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80 Met Ser Thr Pro Arg Phe Ala Leu His Tyr Ala Ser Ala Ser Val Leu
81 1 5 10 15
82 Leu Ala Ala Ser Gly Leu Ala Met Ala Gln Thr Ala Thr Gln Ile His
83 20 25 30
84 Asp Pro Ser Gln Val Gln Gln Met Ala Thr Val Gln Val Leu Gly Thr
85 35 40 45
86 Ala Glu Glu Glu Ile Lys Glu Ser Leu Gly Val Ser Val Ile Thr Ala
87 50 55 60
88 Glu Glu Ile Ala Arg Arg Pro Pro Thr Asn Asp Leu Ser Asp Leu Ile
89 65 70 75 80
90 Arg Arg Glu Pro Gly Val Asn Leu Thr Gly Asn Ser Ala Ser Gly Ala
91 85 90 95
92 Arg Gly Asn Ser Arg Gln Val Asp Ile Arg Gly Met Gly Pro Glu Asn
93 100 105 110
94 Thr Leu Ile Leu Ile Asp Gly Lys Pro Val Thr Ser Arg Asn Ala Val
95 115 120 125
96 Arg Tyr Gly Trp Asn Gly Asp Arg Asp Thr Arg Gly Asp Thr Asn Trp
97 130 135 140
98 Val Pro Ala Glu Glu Val Glu Arg Ile Glu Val Ile Arg Gly Pro Ala
99 145 150 155 160
100 Ala Ala Arg Tyr Gly Ser Gly Ala Met Gly Gly Val Val Asn Ile Ile
101 165 170 175
102 Thr Lys Arg Pro Ala Asp Arg Ala Thr Gly Ser Ile Thr Tyr Thr
103 180 185 190
104 Asn Gln Pro Glu Asp Ser Arg Glu Gly Asn Thr Asn Arg Val Asn Ala
105 195 200 205
106 Arg Ile Ser Ala Pro Ile Ser Asp Thr Leu Ser Met Arg Leu Tyr Gly
107 210 215 220

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108 Asn Tyr Asn Lys Thr Asn Pro Asp Ala Arg Asp Ile Asn Ala Gly His
109 225                230                235                240
110 Ala Asn Thr Ser Asp Asn Gly Asn Pro Ser Thr Ala Gly Arg Glu Gly
111                245                250                255
112 Val Ile Asn Gln Asp Leu Ser Ala Leu Phe Ser Trp Lys Ala Asp Ser
113                260                265                270
114 His Asn Thr Val Asp Leu Asp Met Gly Phe Ser Arg Gln Gly Asn Leu
115                275                280                285
116 Phe Ala Gly Asp Thr Met Asn Asn Ala Asn Ser Asp Phe Ser Asp Ser
117                290                295                300
118 Leu Tyr Gly Lys Glu Thr Asn Ala Met Tyr Arg Glu Asn Tyr Ala Leu
119 305                310                315                320
120 Thr His Arg Gly Val Tyr Asp Trp Gly Thr Ser Arg Ala Ser Val Gly
121                325                330                335
122 Tyr Asp Tyr Thr Arg Asn Ala Arg Gln Arg Glu Gly Leu Ala Gly Gly
123                340                345                350
124 Pro Glu Gly Ala Pro Thr Ala Gly Gly Tyr Asp Thr Ala Arg Leu Lys
125                355                360                365
126 Asn Trp Arg Ala Ala Ala Glu Ala Ser Val Pro Phe His Leu Gly Phe
127                370                375                380
128 Glu Gln Val Ala Thr Val Gly Val Glu Trp Leu Arg Glu Ser Leu Glu
129 385                390                395                400
130 Asp Pro Ala Gly Thr Arg Gln Thr Tyr Thr Gly Gly Ala Ile Gly Gly
131                405                410                415
132 Thr Ala Pro Ala Asp Arg Asp Pro Lys Ser Arg Gln Thr Ser Tyr Ala
133                420                425                430
134 Leu Phe Ala Glu Asp Asn Ile Glu Ile Asp Glu Arg Thr Met Leu Thr
135                435                440                445
136 Pro Gly Val Arg Leu Asp His Asn Ser Glu Phe Gly Ser Asn Trp Ser
137                450                455                460
138 Pro Ser Leu Asn Ala Ser Tyr Ala Val Thr Asp Ala Leu Lys Leu Lys
139 465                470                475                480
140 Gly Gly Ile Ala Arg Ala Tyr Lys Ala Pro Asn Leu Tyr Gln Ser Asn
141                485                490                495
142 Pro Asn Tyr Leu Leu Tyr Ser Arg Gly Asn Gly Cys Leu Ala Ser Gln
143                500                505                510
144 Thr Asn Thr Asn Gly Cys Tyr Leu Val Gly Asn Glu Asp Leu Ser Pro
145                515                520                525
146 Glu Thr Ser Val Asn Lys Glu Ile Gly Phe Glu Tyr Asp Pro Gly Thr
147                530                535                540
148 Trp Arg Thr Ser Met Ala Tyr Phe Arg Asn Asp Tyr Arg Asn Lys Ile
149 545                550                555                560
150 Val Ala Gly Thr Asp Val Gln Tyr Arg Leu Ala Asn Gly Ala Arg Val
151                565                570                575
152 Leu Gln Trp Thr Asn Ser Gly Lys Ala Val Val Glu Gly Leu Glu Gly
153                580                585                590
154 Asn Leu Phe Ile Pro Leu Ala Ser Asn Leu Asp Trp Asn Thr Asn Phe
155                595                600                605
156 Thr Tyr Met Ile Gln Ser Lys Glu Lys Ala Thr Gly Glu Pro Leu Ser

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157      610      615      620
158 Val Ile Pro Glu Tyr Thr Ile Asn Ser Thr Leu Asp Trp Phe Tyr Thr
159 625      630      635      640
160 Pro Gln Leu Ser Phe Gln Ala Asn Leu Thr Tyr Tyr Gly Lys Gln Glu
161      645      650      655
162 Gly Pro Ser Thr Asn Val Arg Thr Gly Val Glu Leu Asn Gly Asp Gly
163      660      665      670
164 Arg Gln Thr Ile Ser Pro Tyr Ala Leu Ala Gly Leu Ser Met Gly Tyr
165      675      680      685
166 Glu Val Asn Arg Asn Leu Lys Phe Arg Val Gly Val Ser Asn Leu Phe
167 690      695      700
168 Asp Lys Gln Leu Tyr Arg Glu Gly Asn Ala Ser Ser Ala Gly Ala Ala
169 705      710      715      720
170 Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Thr Ala Thr Val Ser
171      725      730      735
172 Phe
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 2478
178 <212> TYPE: DNA
179 <213> ORGANISM: Bordetella Pertussis
181 <400> SEQUENCE: 3
182 gtgttttctc gcagtcagaa gcatccgtcc tggcgcctgt cgccatgcgt acttgcggcc 60
183 gccttgtagc cgcgtcgcggt cggtagcgcg gacaccgccc gcgcgcaggc gcccgccgcc 120
184 agcgcccgagc attatgaaat cgcggccgga ccgctggccg acgcactgac ccgcttcgcg 180
185 cgccgtgccc gcgtggtgct gtcgttcgac ccggccctgg tgcaggggcg cagcacggcg 240
186 ggctgtagc gcgtgtacgg cgtgcgcgac gggttcgcg cgctgctggc cggctcgggc 300
187 ctgcaggcgc gcgccggcgg cggcaacaac tggtcgctgg cggcgctgcc gcgcggcggc 360
188 gatgcgcaga cgctggcgcc ggtgacggtg ctgggcctgg agggcgcgct ggcgcccacg 420
189 gtcgggtatg tcgccagtgc cagcctgagc ggcaaccaaga ccgatacgcc gctgacgaa 480
190 acgcccgaat cgatttcggt ggtgactcgc gaccagataa ccgagcaggc cggccagacg 540
191 ctgaaccagg tgctgcgcta taccgccggc gtggcgaccg agacgcgcgg cgcgaccgcg 600
192 acgcggctgg accagttcag cgtgcgcggt ttctccgccc ccacctatct ggacggcatg 660
193 cgctgttctg gcggccggga cgcttgccc caggtcgacg cctaccggct cgaacgggtc 720
194 gatgtgctca aggggcccggc ttccgtgctg tatggccagg gcggcccggg cggcgtggtc 780
195 aaccaggctc gcaagcgtcc cctggacgag cctttgcgcg agatcgaagt gcaggcgggc 840
196 aatttcgatt tccggcgggt caacatggat ttttccggcc cggcggacga ggaccggcgc 900
197 ttctgtacc gggtaaccgg cgcggcctat atgtccgatg gccagggtga tcacaccagg 960
198 gagcgccgct acttcgtctc gccgtcggtc acgtggcggc ccagcgcgga taccacgctg 1020
199 accgtgctga ccaacttcca gcgcgacccc gacatgggtt cgtacggatc gatctcggcc 1080
200 atgcgcacgc tgctgtcggc gcccgcaggc aggcggctgg gcccgaacca ctacgacggc 1140
201 gacgccgatt tcgaaaagag cgaccgccgc agctattcgc tgggctatca actggagcat 1200
202 cgcttcaacg ataccttcaa ggctcgcag aacctgcgtt tccagcatgc cgaggcgctc 1260
203 tatcgcagca tctacggcgc cagcaacaac aattacggct atctcgacaa ggactaccgc 1320
204 tactcgcagc gcggcctggc catcagcgac gtggacgtgg atgcgttcac gatcgacaa 1380
205 aacctgcagg cgcgcttcga taccggggcg ctggcgcata cggcgtggtt ggggttcgac 1440
206 taccagcgcg tgcagacga cacttgctc ggctatggca gcgcggcgcc gctcgacgtg 1500
207 ttcgatccgg actatcacat gggatatcag cggccgccgt ttacgtccga tcagaccag 1560
208 tacaactacc agaccggcct ctacctgcag gaccagatca ggctggatcg cctgtcggtg 1620
209 ctgctgggcg ggcgctacga ctggtcgcgc acccacaccg gcaccgacaa cctggccaac 1680

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210 ggctcgacaca gcagctcggc gctcgccgcc gaggcgttca ccggccgggt cggggcgatc 1740
211 tacaacttcg acaacggcgt ggcgccgtac gccagctact cggagtcgtt cgagccgcag 1800
212 accggcacgg gctggaacaa cagccggttc aagccgaccg aaggcaagca gtatgaggtc 1860
213 ggcgtgaaat accagccgcc gggctcggcc acgctgctca cgctggcggc cttcgacatc 1920
214 cggcgcaaga acctgcccac caccgaccgc gatcccaccc atatgtgcgg cgtttcgcgc 1980
215 tgctcgatac agggccggcga agtgccgacc cgcggcatcg aactggaggc caagaccgaa 2040
216 ccgctgcgcg gcctgagcct gatcgccgcc tattcgctacc tcgacaacga atacgagaag 2100
217 gcctatccga acacgaccgg gttggacctc aagggcaaga agccggtggc cgtgccggcg 2160
218 caccaggcgt cggcctgggc ccgctatcaa ctgcaggagg gcccgcctggc cggcctgggc 2220
219 atgggcgcgg ggggtgcgcta catcggcagt tcgtacgcca acgaaaccaa cacgctcaag 2280
220 gtgccatcgg tgacgctggt ggacatgatg ctgcactacg acctggggccg ggccagcccc 2340
221 gcgctcaagg gcatgcaggg ggcgttgaaac gtctccaacc tgttcgacaa ggaatacatc 2400
222 ggctcgtgcc tgtccgattc gtggtgctgg tatggctacc agcgttcgat caaggccagc 2460
223 ttgcgctatc gctgggtga                                     2478

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225 <210> SEQ ID NO: 4

226 <211> LENGTH: 825

227 <212> TYPE: PRT

228 <213> ORGANISM: Bordetella Pertussis

229 <400> SEQUENCE: 4

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233 Val Leu Ala Ala Ala Leu Cys Ala Val Ala Val Gly Ser Ala Asp Thr
234 20 25 30
235 Ala Arg Ala Gln Ala Pro Ala Ala Ser Ala Gln His Tyr Glu Ile Ala
236 35 40 45
237 Ala Gly Pro Leu Ala Asp Ala Leu Thr Arg Phe Ala Arg Arg Ala Gly
238 50 55 60
239 Val Val Leu Ser Phe Asp Pro Ala Leu Val Gln Gly Arg Ser Thr Ala
240 65 70 75 80
241 Gly Leu Gln Gly Val Tyr Gly Val Arg Asp Gly Phe Ala Ala Leu Leu
242 85 90 95
243 Ala Gly Ser Gly Leu Gln Ala Arg Ala Gly Gly Gly Asn Asn Trp Ser
244 100 105 110
245 Leu Ala Ala Leu Pro Arg Gly Gly Asp Ala Gln Thr Leu Ala Pro Val
246 115 120 125
247 Thr Val Leu Gly Leu Glu Gly Ala Leu Ala Pro Thr Val Gly Tyr Val
248 130 135 140
249 Ala Ser Ala Ser Leu Ser Gly Thr Lys Thr Asp Thr Pro Leu Ile Glu
250 145 150 155 160
251 Thr Pro Gln Ser Ile Ser Val Val Thr Arg Asp Gln Ile Thr Glu Gln
252 165 170 175
253 Gly Ala Gln Thr Leu Asn Gln Val Leu Arg Tyr Thr Ala Gly Val Ala
254 180 185 190
255 Thr Glu Thr Arg Gly Ala Thr Ala Thr Arg Leu Asp Gln Phe Ser Val
256 195 200 205
257 Arg Gly Phe Ser Ala Ala Thr Tyr Leu Asp Gly Met Arg Val Phe Gly
258 210 215 220
259 Gly Arg Asp Ala Leu Pro Gln Val Asp Ala Tyr Arg Leu Glu Arg Val
260 225 230 235 240

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VERIFICATION SUMMARY

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TIME: 12:22:58

Input Set : N:\DA\PTO.DA.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number